



Figure 1A

1 GGAAGTCAGCAGCGCTTGGGAGGGGTGGCGGGGGAATAGCGGGCGCAGC
51 AGCCCCAGCCCTCAGAGACAGCAGAAAGGAGGGAGGGTGCTGG
101 GGGACAGCCCCCACCATTCTACCGCTATGGGCCCCAACCTCCCACTCC
151 CACCTCCCCCTCATCGGCCGGGCTAGGACACCCCCCAAATCCCGTCGCCC
201 CCTTGCCACCGACACCCCGACAGAGACAGAGACAGCCATCCGCCACCA
251 CCGCTGCCGAGCCTGGCTGGGAGGGGCCAGCCCCCAGGCCCTTAC
301 CCCTCTGAGGTGCCAGA ATG GAT TTG TGG CCA GGG GCA TGG
Met Asp Leu Trp Pro Gly Ala Trp
343 ATG CTG CTG CTG CTC TTC CTG CTG CTG CTC TTC C
Met Leu Leu Leu Leu Phe Leu Leu Leu Phe L
20
10
380 TG CTG CCC ACC CTG TGG TTC TGC AGC CCC AGT GCC AAG
eu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys
30

Figure 1B

418 TAC TTC TTC AAG ATG GCC TTC TAC AAT GGC TGG ATC C
Tyr Phe Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile L

40

455 TC TTC CTG GCT GTG CTC GCC ATC CCT GTG TGT GCC GTG
eu Phe Leu Ala Val Leu Ala Ile Pro Val Cys Ala Val

50

493 CGA GGA CGC AAC GTC GAG AAC ATG AAG ATC TTG CGT C
Arg Gly Arg Asn Val Glu Asn Met Lys Ile Leu Arg L

70

60

530 TA ATG CTG CTC CAC ATC AAA TAC CTG TAC GGG ATC CGA
eu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg

80

Figure 1C

568 GTG GAG GTG CGA GGG GCT CAC CAC TTC CCT CCC TCG C
Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser G

90

605 AG CCC TAT GTT GTT GTC TCC AAC CAC CAG AGC TCT CTC
In Pro Tyr Val Val Val Ser Asn His Gln Ser Ser Leu

100

643 GAT CTG CTT GGG ATG ATG GAG GTA CTG CCA GGC CGC T
Asp Leu Leu Gly Met Met Glu Val Leu Pro Gly Arg C

120

110

680 GT GTG CCC ATT GCC AAG CGC GAG CTA CTG TGG GCT GGC
ys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp Ala Gly

130

Figure 1D

718 TCT GCC GGG CTG GCC TGC TGG CTG GCA GGA GTC ATC T
Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile P

140

755 TC ATC GAC CGG AAG CGC ACG GGG GAT GCC ATC AGT GTC
he Ile Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val

150

793 ATG TCT GAG GTC GCC CAG ACC CTG CTC ACC CAG GAC G
Met Ser Glu Val Ala Gln Thr Leu Leu Thr Gln Asp V

170

160

830 TG AGG GTC TGG GTG TTT CCT GAG GGA ACG AGA AAC CAC
al Arg Val Trp Val Phe Pro Glu Gly Thr Arg Asn His

180

Figure 1 E

868 AAT GGC TCC ATG CTG CCC TTC AAA CGT GGC GCC TTC C
Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe H
190

905 AT CTT GCA GTG CAG GCC CAG GTT CCC ATT GTC CCC ATA
is Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile
200

943 GTC ATG TCC TCC TAC CAA GAC TTC TAC TGC AAG AAG G
Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys G
210 220

980 AG CGT CGC TTC ACC TCG GGA CAA TGT CAG GTG CGG GTG
lu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val
230

Figure 1F

1018 CTG CCC CCA GTG CCC ACG GAA GGG CTG ACA CCA GAT G
Leu Pro Pro Val Pro Thr Glu Gly Leu Thr Pro Asp A

240

1055 AC GTC CCA GCT CTG GCT GAC AGA GTC CGG CAC TCC ATG
sp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met

250

1093 CTC ACT GTT TTC CGG GAA ATC TCC ACT GAT GGC CGG G
Leu Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg G

270

260

1130 GT GGT GAC TAT CTG AAG AAG CCT GGG GGC GGT GGG
ly Gly Gly Asp Tyr Leu Lys Lys Pro Gly Gly Gly 280

1168 TGA ACCCTGGCTCTGAGCTCTCCTCCCATCTGTCCCCATCTTCTCTCCC

1216 CACACCTACCCACCCAGTGGGCCCTGAAGCAGGCCCAAACCCCTTCTCCTT

1266 GTCTCCCTCTCCCCACTTATCTCTCTTCTTGGAAATCTTCAACTTCTGAA

Figure 1G

1316 GTGAATGTGGATAACAGGCCACTCCTGCCCCCTCTTGGCCCCATCCATGG
1366 ACTCTTGCCCTCGGTGCAGTTTCCACTCTTGACCCCCACCTCCTACTGTCT
1416 TGTCTGTGGACAGTTGCCCTCCCCCTCATCTCCAGTGA CTAGCCTACAC
1466 AAGGAGGGGAACATTCCATCCCCAGTGGAGTCTCTTCC TATGTGTCTT
1516 CTCTACCCCTCTACCCCCACATTGGCCAGTGGACTCATCCATTCTTTGGA
1566 ACAAATCCCCCCCCACTCCAAGTCCATGGATTCAATGGA CTCA TCCATT
1616 TGTGAGGAGGACTTCTCGCCCTCTGGCTGGAAGCTGATA CCTGAAGCACT
1666 CCCAGGCTCATCCTGGGAGCTTTCCCTCAGCACCTTCA CCTTCCCCTCCAG
1716 TGTAGCCTCCTGTCA GTGGGGCTGGACCCCTTCTAATTCA GAGTCTCAT
1766 GCCTGCCCTTGCC CAGATGCCCCAGGGTCGTGCACTCTCTGGGATACCAGT
1816 TCAGTCTCCACATT TCTGGTTTCTGTCCCCCATAGTACAGTTCTTCAGTG
1866 GACATGACCCCCACCCAGCCCCCTGCAGCCCTGCTGACCATCTCACCAGAC
1916 ACAAGGGGAAGAGCAGACATCAGGTGCTGCACTCACTTCTGCCCCCTGG
1966 GGAGTTGGGGAAGGAACGAACCCCTGGCTGGAGGGGATAGGAGGGCTTTT

Figure 1H

2016 AATTATTTCTTTTCTGTTGAGGCTTCCCCCTCTCTGAGCCAGTTTTC
2066 TTTCTTCCCTGGTGGCATTAGCCACTCCCTGCCTCTCACTCCAGACCTGTT
2116 CCCACAAC TGGGAGGTAGGCTGGGAGCAAAAGGAGAGGGTGGGACCCAG
2166 TTTTCCGTGGTTGGTTTATTATTAATTAATCTGGATAACAGCAAAAAA
2216 AAAATAAGAGAGAGAGAAAAAAA

Figure 2 A

Human LPAAT	1	MDLWPGAWM-	10	20	30	40	50
Yeast LPAAT	1	MSV-IGREFLY	---	LLLLLF	LL-LLFLLP	LWFCSPSAKY	F-----FKMA
E.coli LPAAT	1	M-----	---	LYIF	RL-IITVIYS	ILVCVFGSIY	-----
Maize LPAAT	1	MAI-----	---	PLVLVVL	PLGLLELLSG	LIVNAIQAVL	FVTIRPFESKS
Human LPAAT	51	FYNGWILFLA	60	70	80	90	100
Yeast LPAAT	51	FY-----G	---	VIASILCTLI	GKQHLAQWIT	ARCFYHVMKL	MLGLDV---K
E.coli LPAAT	51	-----	---	-----CLFS	PRNPKHVATF	GHMFGRLAPL	-FGLKVECRK
Maize LPAAT	51	FYRRINRFLA	EL	-----	-----L	WLQLVWVVDW	WAGVKVQLHA
Human LPAAT	101	AHFE-PPSQ-	110	120	130	140	150
Yeast LPAAT	101	VUGE-ENLAK	---	KPYIMIANHQ	SSLDLLGMME	VL--PGRC--	-VPI-AKREL
E.coli LPAAT	101	PTDA-ESYG-	---	-NAIYIANHQ	STLDIFMLGR	IF--PPGCT-	---VTAKKSL
Maize LPAAT	101	DEETYSRMGK	EHALLISNHR	SDIDWL-IGW	ILAQRSGLG	IVQ-PP----	TVTIV-GKKSL
Human LPAAT	151	LWAGSAGLAC	160	170	180	190	200
Yeast LPAAT	151	KYVPFLG---	---	WFMALSGTYF	IDRKRTGDAL	SVMSEVAQTL	LTQDVRVWV-
E.coli LPAAT	151	LWIPFFGQLY	W----	LTGNLL	LDRSKRQEI	DTLNKGLENV	KKNKRALWV-
Maize LPAAT	151	KFLPVIGWSM	WF----	AEYLF	IDRNNRTKAH	GTAIEVVNHF	KKRRISIWM-
Human LPAAT	201	FPEGTRNHN	GS-----	---	---	MLPFFKRGAFH	LAVQAQVPIV
Yeast LPAAT	201	FPEGTRSYT	SEL-----	---	---	MLPFFKRGAFH	LAQCKIPIV
E.coli LPAAT	201	FPEGTRSRG	RGL-----	---	---	-LPFKTGAFH	AAIAAGVPII
Maize LPAAT	201	LFVEGTRFTP	AKLLAAQEYA	ASQGLPAPRN	VLIPRTKGFV	SAVSIMRDFV	---

Figure 2 B

Human LPAAT	251	PIVMSSYQDF	YCKKERFRTS	GQCQVRVLPP	VPTEGLTPDD	VPALADR---
Yeast LPAAT	251	PVVVSNTSTL	VSPKYGVFNR	GCMIVRILKP	ISTENLTCKDK	IGEFAEK---
E.coli LPAAT	251	PVCVSTTSNK	I--NLNRLHN	GLVIVEMLPP	IDVSQYCKDQ	VRELAH---
Maize LPAAT	251	PAIYDTT--V	IVPKDSPQPT	MLRILKGQSS	VIHVRMKRHA	MSEMPKSD
		260	270	280	290	300
Human LPAAT	301	-----	VRHSM TV -F	REISTDGRGG	GDYLKKPGGG	G*.....
Yeast LPAAT	301	-----	VRDQM VD T-L	KEIGYSPAIN	DTTLPPQ---	-----
E.coli LPAAT	301	-----	CRSIMEQK-I	AELDK VE AE-	-----REAAGK	V*.....
Maize LPAAT	301	VSKWCKDIFV	AKDALLDKHL	ATGTFDEEIR	PIGRPVKSLL	VTLFWSCLLL
		310	320	330	340	350
Human LPAAT	351
Yeast LPAAT	351	--AIEY---A	AL-----Q	HDKKVNKKIK	NEPVPSVIS	NDVNTHNEGS
E.coli LPAAT	351
Maize LPAAT	351	FGAIEFFKWT	QLLSTWRGVA	FTAAGMALVT	GVMHVFIMFS	QA-----ERS
		360	370	380	390	400
Human LPAAT	401
Yeast LPAAT	401	S-----V	KKMH*
E.coli LPAAT	401
Maize LPAAT	401	SSARAARNRV	KKE*
		410	420	430	440	450

Figure 3A

10	20	30	40	50	60
GGAGCGAGCT	GGCGGCGCCG	TCGGGCGCCG	GGCCGGGCCA	TGGAGCTGTG	GCCGTGTCTG
70	80	90	100	110	120
GCCGCGGCGC	TGCTGTTGCT	GCTGCTGCTG	GTGCAGCTGA	GCCGCGCGGC	CGAGTTCTAC
130	140	150	160	170	180
GCCAAGGTCTG	CCCTGTACTG	CGCGCTGTGC	TTCACGGTGT	CCGCCGTGGC	CTCGCTCGTC
190	200	210	220	230	240
TGCCTGCTGT	GCCACGGCGG	CCGGACGGTG	GAGAACATGA	GCATCATCGG	CTGGTTCTGTG
250	260	270	280	290	300
CGAAGCTTCA	AGTACTTTTA	CGGGCTCCGC	TTCGAGGTGC	GGGACCCGCG	CAGGCTGCAG
310	320	330	340	350	360
GAGGCCCGTC	CCTGTGTCAT	CGTCTCCAAC	CACCAGAGCA	TCCTGGACAT	GATGGGCCCTC
370	380	390	400	410	420
ATGGAGGTCC	TTCCGGAGCG	CTGCGTGCAG	ATCGCCAAGC	GGGAGCTGCT	CTTCCTGGGG
430	440	450	460	470	480
CCCGTGGGCC	TCATCATGTA	CCTCGGGGGC	GTCTTCTTCA	TCAACCGGCA	GCGCTCTAGC
490	500	510	520	530	540
ACTGCCATGA	CAGTGATGGC	CGACCTGGGC	GAGCGCATGG	TCAGGGAGAA	CCTCAAAGTG

Figure 3B

550	560	570	580	590	600
TGGATCTATC	CCGAGGGTAC	TCGCAACGAC	AATGGGACC	TGCTGCCCTTT	TAAGAAGGGC
610	620	630	640	650	660
GCCTTCTACC	TGGCAGTCCA	GGCACAGGTG	CCCATCGTCC	CCGTGGTGTA	CTCTTCCCTC
670	680	690	700	710	720
TCCTCCTTCT	ACAACACCAA	GAAGAAGTTC	TTCACCTTCAG	GAACAGTCAC	AGTGCAGGTG
730	740	750	760	770	780
CTGGAAGCCA	TCCCCACCAG	CGGCCTCACT	GCGGCGGACG	TCCCTGGGCT	CGTGGACACC
790	800	810	820	830	840
TGCCACCGGG	CCATGAGGAC	CACCTTCCTC	CACATCTCCA	AGACCCCCCA	GGAGAACGGG
850	860	870	880	890	900
GCCACTGCGG	GGTCTGGCGT	GCAGCCGGCC	CAGTAGCCCA	GACCACGGCA	GGGCATGACC
910	920	930	940	950	960
TGGGGAGGGC	AGGTGGAAGC	CGATGGCTGG	AGGATGGGCA	GAGGGGACTC	CTCCCCGGCTT
970	980	990	1000	1010	1020
CCAAATACCA	CTCTGTCCGG	CTCCCCCAGC	TCTCACTCAG	CCCGGAAGC	AGGAAGCCCC
1030	1040	1050	1060	1070	1080
TTCTGTCACT	GGTCTCAGAC	ACAGGCCCCCT	GGTGTCCCCT	GCAGGGGGCT	CAGCTGGACC

Figure 3C

1090	1100	1110	1120	1130	1140
CTCCCCGGC	TCGAGGGCAG	GGA	CTCGGC	CTCTGGNGCT	GGGNTGATAA
1150	1160	1170	1180	1190	1200
AGATGAGGCT	TGCGGCTGTG	GCCCGCTGGT	GGGCTGAGCC	ACAAGGCCCC	CGATGGCCCA
1210	1220	1230	1240	1250	1260
GGAGCAGATG	GGAGGACCCC	GAGGCCAGGA	GTCCCAGACT	CACGCACCCCT	GGGCCACAGG
1270	1280	1290	1300	1310	1320
GAGCCGGGAA	TCGGGGCCCTG	CTGCTCCTGC	TGGCCTGAAG	AATCTGTGGG	GTCAGCACTG
1330	1340	1350	1360	1370	1380
TACTCCGTTG	CTGTTTTTTT	ATAAACACAC	TCTTGGA	AAAAA	AAAAA
1390	1400	1410	1420	1430	1440
AAA.....

Figure 4A

10	20	30	40	50
GGAGCGAGCTGGCGCGCGCTCGGCGCGCGCGCGGCC	ATG	GAG	CTG	TGG CCG
	Met	Glu	Leu	Trp Pro
60	70	80	90	
TGT CTG GCC GCG GCG CTG CTG TTG CTG CTG CTG	CTG	GAG	CTG	CAG CTG
Cys Leu Ala Ala Ala Leu Leu Leu Leu Leu	Val	Gln	Leu	20
100	110	120	130	140
AGC CGC GCG GCC GAG TTC TAC GCC AAG GTC GCC	CTG	TAC	TGC	GCG
Ser Arg Ala Ala Ala Glu Phe Tyr Ala Lys	Val	Ala	Leu	Tyr Cys Ala
				30
150	160	170	180	
CTG TGC TTC ACG GTG TCC GCC GTG GCC TCG CTC	GTC	TGC	CTG	CTG
Leu Cys Phe Thr Val Ser Ala Val Ala Ser	Leu	Val	Cys	Leu
				50
190	200	210	220	230
TGC CAC GGC GGC CGG ACG GTG GAG AAC ATG	AGC	ATC	ATC	GGC TGG
Cys His Gly Gly Arg Thr Val Glu Asn	Met	Ser	Ile	Ile Gly Trp
				60

Figure 4B

240	TTC GTG CGA AGC TTC AAG TAC TTT TAC GGG CTC CGC TTC GAG GTG	260	270	280
	Phe Val Arg Ser Phe Lys Tyr Phe Tyr Gly Leu Arg Phe Glu Val			80
		250		
		70		
290	CGG GAC CCG CGC AGG CTG CAG GAG GCC CGT CCC TGT GTC ATC GTC	310	320	
	Arg Asp Pro Arg Arg Leu Gln Glu Ala Arg Pro Cys Val Ile Val			
		300		
		90		
330	TCC AAC CAC CAG AGC ATC CTG GAC ATG ATG GGC CTC ATG GAG GTC	350	360	
	Ser Asn His Gln Ser Ile Leu Asp Met Met Gly Leu Met Glu Val			110
		340		
		100		
370	CTT CCG GAG CGC TGC GTG CAG ATC GCC AAG CGG GAG CTC ATG CTC TTC	400	410	
	Leu Pro Glu Arg Cys Val Gln Ile Ala Lys Arg Glu Leu Phe			
		390		
		120		
420	CTG GGG CCC GTG GGC CTC ATC ATG TAC CTC GGG GGC GTC TTC TTC	440	450	
	Leu Gly Pro Val Gly Leu Ile Met Tyr Leu Gly Gly Val Phe			140
		430		
		130		
460	ATC AAC CGG CAG CGC TCT AGC ACT GCC ATG ACA GTG ATG GCC GAC	480	490	
	Ile Asn Arg Gln Arg Ser Thr Ala Met Thr Val Met Ala Asp			500
		470		
		150		

Figure 4C

510	520	530	540	
CTG GGC GAG CGC ATG GTC AGG GAG AAC CTC AAA GTG TGG ATC TAT				
Leu Gly Glu Arg Met Val Arg Glu Asn Leu Lys Val Trp Ile Tyr				170
160				
550	560	570	580	590
CCC GAG GGT ACT CGC AAC GAC AAT GGG GAC CTG CTG CCT TTT AAG				
Pro Glu Gly Thr Arg Asn Asp Asn Gly Asp Leu Leu Pro Phe Lys				
				180
600	610	620	630	
AAG GGC GCC TTC TAC CTG GCA GTC CAG GCA CAG GTG CCC ATC GTC				
Lys Gly Ala Phe Tyr Leu Ala Val Gln Ala Gln Val Pro Ile Val				200
190				
640	650	660	670	680
CCC GTG GTG TAC TCT TCC TTC TCC TCC TTC TAC AAC ACC AAG AAG				
Pro Val Val Tyr Ser Ser Phe Ser Ser Phe Tyr Asn Thr Lys Lys				
			210	
690	700	710	720	
AAG TTC TTC ACT TCA GGA ACA GTC ACA GTG CAG GTG CTG GAA GCC				
Lys Phe Phe Thr Ser Gly Thr Val Thr Val Gln Val Leu Glu Ala				230
				220

Figure 4 D

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730          740          750          760          770
ATC CCC ACC AGC GGC CTC ACT GCG GCG GAC GTC CCT GCG CTC GTG
Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp Val Pro Ala Leu Val
240

780          790          800          810
GAC ACC TGC CAC CGG GCC ATG AGG ACC ACC TTC CTC CAC ATC TCC
Asp Thr Cys His Arg Ala Met Arg Thr Thr Phe Leu His Ile Ser
250

820          830          840          850          860
AAG ACC CCC CAG GAG AAC GGG GCC ACT GCG GGG TCT GGC GTG CAG
Lys Thr Pro Gln Glu Asn Gly Ala Thr Ala Gly Ser Gly Val Gln
270

870          880          890          900          910          920
CCG GCC CAG TAG CCCAGACCAGGAGGACTCCTCCGGCTTCCAATACCACCTCTGTCCGG
Pro Ala Gln **

930          940          950          960          970          980
CGATGGCTGGAGGATGGGCAGAGGGGACTCCTCCGGCTTCCAATACCACCTCTGTCCGG

990          1000          1010          1020          1030          1040
CTCCCCCAGCTCTCACTCAGCCCGGGAAGCAGGAAGCCCTTCTGTCACTGGTCTCAGAC
1050          1060          1070          1080          1090          1100
ACAGGCCCTGTGTCCCTGCAGGGGGCTCAGCTGGACCCCTCCCGGGCTCGAGGGCAG
```

Figure 4 E

1110	1120	1130	1140	1150	1160
	GGACTCGCGCC	CACGGCACCTCT	GGNGCTGGNTGATA	AAAGATGAGGCT	TGCGGCTGTG
1170	1180	1190	1200	1210	1220
	GCCCGCTGGT	GGCTGAGCCACA	AGCCCCCGATG	CCCCAGGAGCAGAT	GGGAGGACCCC
1230	1240	1250	1260	1270	1280
	GAGGCCAGGAG	TCCCAGACTCAC	GCACCCCTGGCC	CACAGGAGCCGGA	ATCGGGGCCTG
1290	1300	1310	1320	1330	1340
	CTGCTCCTGCT	GGCCTGAAGAA	TCTGTGGGT	CAGCAGTGTACT	CCGTTGCTGTTTTT
1350	1360	1370	1380		
	ATAAACACACTCTTGGAAAAA				

Figure 5 A

Alignment of LPAAT Sequences.

		10	20	30	40	50
Human LPAAT- β	1	-----	-----	MEL WPC-----	LA AALLLLLV	
Human LPAAT- α	1	-----	-----	MDL WPGAWLLLL	LEFLLLFLLP	
Yeast LPAAT	1	-----	-----	MSV --IGRFLYL	RSVLWLALA	
E.coli LPAAT	1	-----	-----	-----	-----	
H.influenzae	1	-----	-----	-----	-----	
S.typhimurium	1	-----	-----	-----	-----	
L.douglasi	1	MAKIRTS--L	RNR-----	-----	RQLKP AVAATAD--D	DKDGVFMV--
C. nificera	1	MDASCASSFL	RGRCLESCFK	ASFGMSQPKD	AAGQPSRRPA	DADDFFTVDD
Human LPAAT- β	51	QL---	SRAAE FYAKVAL-YC	ALCFTVSAVA	SLVCLLCHGG	RTVENM-SII
Human LPAAT- α	51	TLWFCSRSAK	YFFKMAF--YN	GWILFLAVLA	IPVCAV--RG	RNVENM-KIL
Yeast LPAAT	51	G---CG---	FY-----	-----	GVIA SILCTLIKQ	HLAQWI-TAR
E.coli LPAAT	51	-----	MLYI	FRLITVIYS	ILVC---VFG	SIYCLFSPRN PKHV---ATF
H.influenzae	51	-----	MLKL	LRIFLMLIC	ILIC---VLG	TIYSFIREKN PSNV---GIV
S.typhimurium	51	-----	MLYI	FRLITVIYS	ILVC---VFG	SIYCLFSPRN PKHV---ATF
L.douglasi	51	-----	LLSC	FKIFVCFEFT	WLTAVANG	LIMVLLLPW YMRIRLGNLY
C. nificera	51	DRWTIVILSV	VRIACFL--	SMWTTIVN	MIMILLPWP	YARIRQGNLY

Figure 5 B

	110	120	130	140	150
Human LPAAT- β	101 <u>GW</u> <u>FV</u> <u>RS</u> <u>FK</u> -	-- <u>FY</u> <u>GR</u> <u>FE</u> <u>V</u>	<u>RD</u> <u>PR</u> <u>RL</u> <u>Q</u> <u>EA</u> <u>R</u>	<u>PC</u> <u>VI</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>I</u> <u>LD</u> <u>M</u> <u>G</u> <u>LM</u> <u>GE</u> <u>V</u>
Human LPAAT- α	101 <u>RL</u> <u>ML</u> <u>I</u> <u>H</u> <u>I</u> <u>K</u> <u>Y</u> -	-- <u>LY</u> <u>G</u> <u>IR</u> <u>VE</u> <u>V</u>	<u>RG</u> <u>AH</u> <u>FP</u> <u>PS</u> <u>Q</u>	<u>PV</u> <u>VV</u> <u>VS</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>S</u> <u>LD</u> <u>IL</u> <u>G</u> <u>MM</u> <u>EV</u>
Yeast LPAAT	101 <u>CF</u> <u>Y</u> <u>-H</u> <u>VM</u> <u>KL</u> -	-- <u>ML</u> <u>GL</u> <u>D</u> <u>V</u> <u>K</u> <u>V</u>	<u>VG</u> <u>EE</u> <u>N</u> <u>L</u> <u>A</u> <u>K</u> <u>-K</u>	<u>PY</u> <u>IM</u> <u>I</u> <u>A</u> <u>NH</u> <u>Q</u> <u>S</u>	<u>T</u> <u>LD</u> <u>I</u> <u>F</u> <u>ML</u> <u>GR</u> <u>I</u>
E.coli LPAAT	101 <u>GH</u> <u>MF</u> <u>GR</u> <u>L</u> ---	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PT</u> <u>DA</u> <u>ES</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>I</u> <u>A</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AS</u> <u>NI</u>
H.influenzae	101 <u>AR</u> <u>WF</u> <u>GR</u> <u>L</u> - <u>FT</u>	<u>Y</u> <u>PL</u> <u>F</u> <u>GL</u> <u>K</u> <u>VE</u> <u>H</u>	<u>RI</u> <u>PQ</u> <u>D</u> <u>X</u> <u>Q</u> <u>IS</u>	<u>RA</u> <u>IY</u> <u>I</u> <u>G</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>IS</u> <u>YM</u>
S.typhimurii	101 <u>GH</u> <u>MF</u> <u>GR</u> <u>L</u> - <u>FT</u>	<u>AP</u> <u>LF</u> <u>GL</u> <u>K</u> <u>VE</u> <u>C</u>	<u>RK</u> <u>PA</u> <u>DA</u> <u>EN</u> <u>Y</u> <u>G</u>	<u>NA</u> <u>IY</u> <u>I</u> <u>A</u> <u>NH</u> <u>Q</u> <u>N</u>	<u>NY</u> <u>DM</u> <u>VT</u> <u>AN</u> <u>NI</u>
L.douglasi	101 <u>CH</u> <u>I</u> <u>I</u> <u>CG</u> <u>LV</u> --	<u>IW</u> <u>IY</u> <u>G</u> <u>I</u> <u>P</u> <u>I</u> <u>K</u>	<u>QG</u> <u>SE</u> <u>H</u> <u>I</u> <u>K</u> <u>K</u> <u>RA</u>	<u>IFT</u> <u>Y</u> <u>I</u> <u>S</u> <u>NH</u> <u>AS</u>	<u>P</u> <u>IDA</u> <u>FF</u> <u>VM</u> <u>WL</u>
C. nucifera	101 <u>CH</u> <u>VT</u> <u>GR</u> <u>ML</u> <u>FT</u>	<u>MW</u> <u>IL</u> <u>GN</u> <u>P</u> <u>ITI</u>	<u>EG</u> <u>SE</u> <u>FS</u> <u>N</u> <u>TR</u> <u>A</u>	<u>I</u> -- <u>Y</u> <u>IC</u> <u>NH</u> <u>AS</u>	<u>LD</u> <u>VI</u> <u>FL</u> <u>IM</u> <u>WL</u>
	160	170	180	190	200
Human LPAAT- β	151 <u>LP</u> <u>ER</u> <u>CV</u> <u>Q</u> <u>IAK</u>	<u>RE</u> <u>LL</u> <u>FL</u> <u>GP</u> <u>V</u> -	<u>GL</u> <u>IM</u> <u>Y</u> <u>LG</u> <u>V</u>	<u>FF</u> <u>IN</u> <u>R</u> <u>Q</u> <u>RS</u> <u>ST</u>	<u>AM</u> <u>T</u> -- <u>VM</u> <u>AD</u> <u>L</u>
Human LPAAT- α	151 <u>LP</u> <u>GR</u> <u>CV</u> <u>PIAK</u>	<u>RE</u> <u>LL</u> <u>W</u> <u>AG</u> <u>SA</u> -	<u>GL</u> <u>AC</u> <u>W</u> <u>L</u> <u>AG</u> <u>V</u>	<u>IF</u> <u>ID</u> <u>R</u> <u>K</u> <u>R</u> <u>T</u> <u>GD</u>	<u>AI</u> <u>S</u> -- <u>VM</u> <u>SE</u> <u>V</u>
Yeast LPAAT	151 <u>FP</u> <u>PG</u> <u>CT</u> <u>VTAK</u>	<u>KS</u> <u>LK</u> <u>V</u> <u>PF</u> <u>L</u> -	<u>GW</u> <u>F</u> <u>MA</u> <u>LS</u> <u>GT</u>	<u>YF</u> <u>LD</u> <u>RS</u> <u>K</u> <u>R</u> <u>Q</u> <u>E</u>	<u>AI</u> <u>D</u> -- <u>T</u> <u>IN</u> <u>K</u> <u>G</u>
E.coli LPAAT	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>VGK</u>	<u>KS</u> <u>LL</u> <u>WI</u> <u>PI</u> <u>FF</u> -	<u>GQ</u> <u>LY</u> <u>WL</u> <u>T</u> <u>GN</u>	<u>LL</u> <u>ID</u> <u>R</u> <u>NN</u> <u>R</u> <u>TK</u>	<u>AH</u> <u>G</u> -- <u>T</u> <u>IA</u> <u>EV</u>
H.influenzae	151 <u>VQ</u> <u>PR</u> <u>IV</u> <u>SVGK</u>	<u>KS</u> <u>LI</u> <u>WI</u> <u>PI</u> <u>FF</u> <u>FF</u>	<u>TG</u> <u>LY</u> <u>W</u> <u>VT</u> <u>GN</u>	<u>IF</u> <u>LD</u> <u>EN</u> <u>R</u> <u>TK</u>	<u>AH</u> <u>N</u> -- <u>T</u> <u>MS</u> <u>QL</u>
S.typhimurii	151 <u>VQ</u> <u>PT</u> <u>VT</u> <u>VGK</u>	<u>KS</u> <u>LL</u> <u>WI</u> <u>PI</u> <u>FF</u> <u>FF</u>	<u>TG</u> <u>Q</u> <u>LY</u> <u>WL</u> <u>T</u> <u>GN</u>	<u>LL</u> <u>ID</u> <u>R</u> <u>NN</u> <u>RAK</u>	<u>AH</u> <u>S</u> -- <u>T</u> <u>IA</u> <u>AV</u>
L.douglasi	151 <u>AP</u> <u>IG</u> <u>TV</u> <u>GVAK</u>	<u>KE</u> <u>VI</u> <u>W</u> <u>Y</u> <u>P</u> <u>IL</u> <u>G</u>	<u>Q</u> -- <u>LY</u> <u>T</u> <u>LAH</u>	<u>IR</u> <u>ID</u> <u>RS</u> <u>N</u> <u>PAA</u>	<u>AI</u> <u>Q</u> <u>S</u> <u>FT</u> <u>M</u> <u>KEA</u>
C. nucifera	151 <u>IP</u> <u>K</u> <u>G</u> <u>TV</u> <u>T</u> <u>IAK</u>	<u>KE</u> <u>II</u> <u>W</u> <u>Y</u> <u>P</u> <u>LF</u> <u>G</u>	<u>Q</u> <u>FT</u> <u>LY</u> <u>V</u> <u>LAH</u>	<u>QR</u> <u>ID</u> <u>RS</u> <u>N</u> <u>PSA</u>	<u>AI</u> <u>ES</u> -- <u>I</u> <u>KE</u> <u>V</u>

Figure 5C

Human LPAAT-β	201	GERMRENK	210	220	230	240	250
Human LPAAT-α	201	AQTLLTQDVR	210	220	230	240	250
Yeast LPAAT	201	LENVKKNKRA	210	220	230	240	250
E.coli LPAAT	201	VNHFKKRRIS	210	220	230	240	250
H.influenzae	201	ARRINEDNLS	210	220	230	240	250
S.typhimurii	201	VNHFKKRRIS	210	220	230	240	250
L.douglassi	201	VRVITEKNLS	210	220	230	240	250
C. nucifera	201	ARAWKKNLS	210	220	230	240	250
Human LPAAT-β	251	VYSSFSS--F	260	270	280	290	300
Human LPAAT-α	251	VMSSYQD--F	260	270	280	290	300
Yeast LPAAT	251	VVSNTST--L	260	270	280	290	300
E.coli LPAAT	251	CVSTTS----	260	270	280	290	300
H.influenzae	251	VCSSTH----	260	270	280	290	300
S.typhimurii	251	CVSNTS----	260	270	280	290	300
L.douglassi	251	ILTGTHLAWF	260	270	280	290	300
C. nucifera	251	VLGTGLAW--	260	270	280	290	300

Figure 5D

	310	320	330	340	350
Human LPAAT- β	301 <u>AMRTT</u> <u>FIHIS</u>	<u>KIPQENGATA</u>	<u>GSGVQPAQ</u> *	-----	-----
Human LPAAT- α	301 <u>SMLT</u> <u>VFREIS</u>	<u>TDCRGGDYL</u>	<u>KPFGGG</u> *	-----	-----
Yeast LPAAT	301 <u>QMVDILKEIG</u>	<u>YSPAINDTTL</u>	<u>PPQAIEYAAL</u>	<u>QHDKKVNKKI</u>	<u>KNEPVPSVSI</u>
E.coli LPAAT	301 <u>-SIMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER</u>	<u>FAACKV</u> *	-----
H.influenzae	301 <u>TDLMEKRIAE</u>	<u>LDEEIA</u>	-----	<u>KGN</u> *	-----
S.typhimuriu	301 <u>TALMEQKIAE</u>	<u>LDKEVA</u>	<u>-ER</u>	<u>EATGKV</u> *	-----
L.douglassi	301 <u>IYVRNLPAQ</u>	<u>KPLGS</u>	<u>-TNR</u>	<u>-S-K</u> *	-----
C. nucifera	301 <u>TALYVDHLPE</u>	<u>SQKPLVSKGR</u>	<u>DASGRNS</u> *	-----	-----
	360	370	380	390	
Human LPAAT- β	351 -----	-----	-----	-----	-----
Human LPAAT- α	351 -----	-----	-----	-----	-----
Yeast LPAAT	351 <u>SNDVNIHNEG</u>	<u>SSVKKMH</u> *	-----	-----	-----
E.coli LPAAT	351 -----	-----	-----	-----	-----
H.influenzae	351 -----	-----	-----	-----	-----
S.typhimuriu	351 -----	-----	-----	-----	-----
L.douglassi	351 -----	-----	-----	-----	-----
C. nucifera	351 -----	-----	-----	-----	-----

Figure 9 A

TCTATGAAACCAACATACATGGCGTTTGCATCACAGTTGGAGTCAGATGTGAGCCCGGAG	60
GGCAGGTGTCTGGCTTGTCCACCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGC	120
TGACCTTGTGCCTTGGACGGCTGTCCTCAGCGAGGGGCCGTGCACCCGCTCCTGAGCAGC	180
GCC ATG GGC CTG CTG GCC TTC CTG AAG ACC CAG TTC GTG CTG CAC	225
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His	
5 10	
CTG CTG GTC GGC TTT GTC TTC GTG GTG AGT GGT CTG GTC ATC AAC	270
Leu Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn	
15 20 25	
TTC GTC CAG CTG TGC ACG CTG GCG CTC TGG CCG GTC AGC AAG CAG	315
Phe Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln	
30 35 40	
CTC TAC CGC CGC CTC AAC TGC CGC CTC GCA TAC TCA CTC TGG AGC	360
Leu Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser	
45 50 55	
CAA CTG GTC ATG CTG CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA	405
Gln Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr	
60 65 70	
CTG TTC ACG GAC CAG GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC	450
Leu Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His	
75 80 85	
GCA GTC ATC ATC CTC AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT	495
Ala Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys	
90 95 100	
GGG TGG ACC ATG TGT GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG	540
Gly Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys	
105 110 115	
GTC CTC GCT AAG AAG GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG	585
Val Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp	
120 125 130	
ACG TGG TAC TTT CTG GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG	630
Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu	
135 140 145	
GAG GAC CGG GAC ACC GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC	675
Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp	
150 155 160	
TAC CCC GAG TAC ATG TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC	720
Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg	
165 170 175	
TTC ACG GAG ACC AAG CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT	765
Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala	
180 185 190	
AAG GGG CTT CCT GTC CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG	810
Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys	
195 200 205	
GGC TTC ACC ACC GCA GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT	855
Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala	
210 215 220	
GTC TAT GAT GTA ACC CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC	900
Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
CTG CTG GGG ATC CTC TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC	945
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys	
240 245 250	
GTG AGG AGA TTT CCT CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA	990
Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu	
255 260 265	
GCA GCT CAG TGG CTT CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC	1035

Figure 10A

CACGCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCCTCAACTGCCCGCTCGCC	61
TACTCACTCTGGAGCCTAGCACAAAAGTAGAAGCAACCCCAAGCACCTGTCACTGGAGACT	121
AATTATGCGGCACCCATACAGGGACCCTCTGCGGCCATCATGGAGAGCCTTCATCTTGCC	181
CGTACAGTTTAAAGCGAAAAAGGAAGTATACAACAAAGTCCATAACTGGTC ATG CTG	238
Met Leu	
CTG GAG TGG TGG TCC TGC ACG GAG TGT ACA CTG TTC ACG GAC CAG	283
Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln	
5 10 15	
GCC ACG GTA GAG CGC TTT GGG AAG GAG CAC GCA GTC ATC ATC CTC	328
Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu	
20 25 30	
AAC CAC AAC TTC GAG ATC GAC TTC CTC TGT GGG TGG ACC ATG TGT	373
Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys	
35 40 45	
GAG CGC TTC GGA GTG CTG GGG AGC TCC AAG GTC CTC GCT AAG AAG	418
Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys	
50 55 60	
GAG CTG CTC TAC GTG CCC CTC ATC GGC TGG ACG TGG TAC TTT CTG	463
Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu	
65 70 75	
GAG ATT GTG TTC TGC AAG CGG AAG TGG GAG GAG GAC CGG GAC ACC	508
Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr	
80 85 90	
GTG GTC GAA GGG CTG AGG CGC CTG TCG GAC TAC CCC GAG TAC ATG	553
Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met	
95 100 105	
TGG TTT CTC CTG TAC TGC GAG GGG ACG CGC TTC ACG GAG ACC AAG	598
Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys	
110 115 120	
CAC CGC GTT AGC ATG GAG GTG GCG GCT GCT AAG GGG CTT CCT GTC	643
His Arg Val Ser Met Glu Val Ala Ala Ala Lys Gly Leu Pro Val	
125 130 135	
CTC AAG TAC CAC CTG CTG CCG CGG ACC AAG GGC TTC ACC ACC GCA	688
Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly Phe Thr Thr Ala	
140 145 150	
GTC AAG TGC CTC CGG GGG ACA GTC GCA GCT GTC TAT GAT GTA ACC	733
Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val Tyr Asp Val Thr	
155 160 165	
CTG AAC TTC AGA GGA AAC AAG AAC CCG TCC CTG CTG GGG ATC CTC	778
Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu Leu Gly Ile Leu	
170 175 180	
TAC GGG AAG AAG TAC GAG GCG GAC ATG TGC GTG AGG AGA TTT CCT	823
Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg Arg Phe Pro	
185 190 195	
CTG GAA GAC ATC CCG CTG GAT GAA AAG GAA GCA GCT CAG TGG CTT	868
Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln Trp Leu	
200 205 210	
CAT AAA CTG TAC CAG GAG AAG GAC GCG CTC CAG GAG ATA TAT AAT	913
His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr Asn	
215 220 225	
CAG AAG GGC ATG TTT CCA GGG GAG CAG TTT AAG CCT GCC CGG AGG	958
Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg	
230 235 240	
CCG TGG ACC CTC CTG AAC TTC CTG TCC TGG GCC ACC ATT CTC CTG	1003
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
245 250 255	
TCT CCC CTC TTC AGT TTT GTC TTG GGC GTC TTT GCC AGC GGA TCA	1048
Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser	

Figure 10 B

	260		265		270		
CCT CTC CTG ATC CTG ACT TTC TTG GGG TTT GTG GGA GCA GCT TCC							1093
Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser							
	275		280		285		
TTT GGA GTT CGC AGA CTG ATA GGA GTA ACT GAG ATA GAA AAA GGC							1138
Phe Gly Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly							
	290		295		300		
TCC AGC TAC GGA AAC CAA GAG TTT AAG AAA AAG GAA TAA TTAATGGC							1185
Ser Ser Tyr Gly Asn Gln Glu Phe Lys Lys Lys Glu ***							
	305		310				
TGTGACTGAACACACGCGGCCCTGACGGTGGTATCCAGTTAACTCAAAACCAACACACAG							1245
AGTGCAGGAAAAGACAATTAGAACTATTTTTCTTATTAAGTGGTGACTAATATTAACAA							1305
AACTTGAGCCAAGAGTAAAGAATTCAGAAGGCCTGTCAGGTGAAGTCTTCAGCCTCCCAC							1365
AGCGCAGGGTCCCAGCATCTCCACGCGCGCCCGTGGGAGGTGGGTCCGGCCGGAGAGGCC							1425
TCCCGCGGACGCGTCTCTCCAGAACTCCGCTTCCAAGAGGGACCTTTGGCTGCTTTCTC							1485
TCCTTAAACTTAGATCAAATTTTAAAAAAAAAAAAAAAA							1523

Figure 11A

TGA	ACC	CAG	CGG	CTC	ATC	TCT	CAG	CTT	CTG	TTT	CTA	AAG	TCC	ATG	TG	CCAA	AGG	CTG	CCAG	61
GA	AGG	A	G	A	C	G	C	T	T	C	T	G	A	T	C	T	T	C	T	121
TA	G	T	T	A	T	T	T	T	C	T	G	A	A	T	C	T	T	T	G	175
Met	Asp	Leu	Ala	Gly	Leu															
CTG	AAG	TCT	CAG	TTC	CTG	TGC	CAC	CTG	GTC	TTC	TGC	TAC	GTC	TTT						220
Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val	Phe	Cys	Tyr	Val	Phe						
			10					15					20							
ATT	GCC	TCA	GGG	CTA	ATC	ATC	AAC	ACC	ATT	CAG	CTC	TTC	ACT	CTC						265
Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln	Leu	Phe	Thr	Leu						
			25					30					35							
CTC	CTC	TGG	CCC	ATT	AAC	AAG	CAG	CTC	TTC	CGG	AAG	ATC	AAC	TGC						310
Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys	Ile	Asn	Cys						
			40					45					50							
AGA	CTG	TCC	TAT	TGC	ATC	TCA	AGC	CAG	CTG	GTG	ATG	CTG	CTG	GAG						355
Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu	Leu	Glu						
			55					60					65							
TGG	TGG	TCG	GGC	ACG	GAA	TGC	ACC	ATC	TTC	ACG	GAC	CCG	CGC	GCC						400
Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg	Ala						
			70					75					80							
TAC	CTC	AAG	TAT	GGG	AAG	GAA	AAT	GCC	ATC	GTG	GTT	CTC	AAC	CAC						445
Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His						
			85					90					95							
AAG	TTT	GAA	ATT	GAC	TTT	CTG	TGT	GGC	TGG	AGC	CTG	TCC	GAA	CGC						490
Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg						
			100					105					110							
TTT	GGG	CTG	TTA	GGG	GGC	TCC	AAG	GTC	CTG	GCC	AAG	AAA	GAG	CTG						535
Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu						
			115					120					125							
GCC	TAT	GTC	CCA	ATT	ATC	GGC	TGG	ATG	TGG	TAC	TTC	ACC	GAG	ATG						580
Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	Trp	Tyr	Phe	Thr	Glu	Met						
			130					135					140							
GTC	TTC	TGT	TCG	CGC	AAG	TGG	GAG	CAG	GAT	CGC	AAG	ACG	GTT	GCC						625
Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	Asp	Arg	Lys	Thr	Val	Ala						
			145					150					155							
ACC	AGT	TTG	CAG	CAC	CTC	CGG	GAC	TAC	CCC	GAG	AAG	TAT	TTT	TTC						670
Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	Pro	Glu	Lys	Tyr	Phe	Phe						
			160					165					170							
CTG	ATT	CAC	TGT	GAG	GGC	ACA	CGG	TTC	ACG	GAG	AAG	AAG	CAT	GAG						715
Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	Thr	Glu	Lys	Lys	His	Glu						
			175					180					185							
ATC	AGC	ATG	CAG	GTG	GCC	CGG	GCC	AAG	GGG	CTG	CCT	CGC	CTC	AAG						760
Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	Gly	Leu	Pro	Arg	Leu	Lys						
			190					195					200							
CAT	CAC	CTG	TTG	CCA	CGA	ACC	AAG	GGC	TTC	GCC	ATC	ACC	GTG	AGG						805
His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	Phe	Ala	Ile	Thr	Val	Arg						
			205					210					215							
AGC	TTG	AGA	AAT	GTA	GTT	TCA	GCT	GTA	TAT	GAC	TGT	ACA	CTC	AAT						850
Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	Tyr	Asp	Cys	Thr	Leu	Asn						
			220					225					230							
TTC	AGA	AAT	AAT	GAA	AAT	CCA	ACA	CTG	CTG	GGA	GTC	CTA	AAC	GGA						895
Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	Leu	Gly	Val	Leu	Asn	Gly						
			235					240					245							
AAG	AAA	TAC	CAT	GCA	GAT	TTG	TAT	GTT	AGG	AGG	ATC	CCA	CTG	GAA						940
Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	Arg	Arg	Ile	Pro	Leu	Glu						
			250					255					260							
GAC	ATC	CCT	GAA	GAC	GAT	GAC	GAG	TGC	TCG	GCC	TGG	CTG	CAC	AAG						985
Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	Ser	Ala	Trp	Leu	His	Lys						
			265					270					275							

Figure 11 B